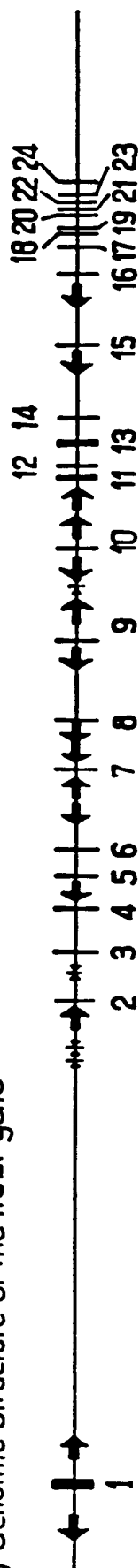


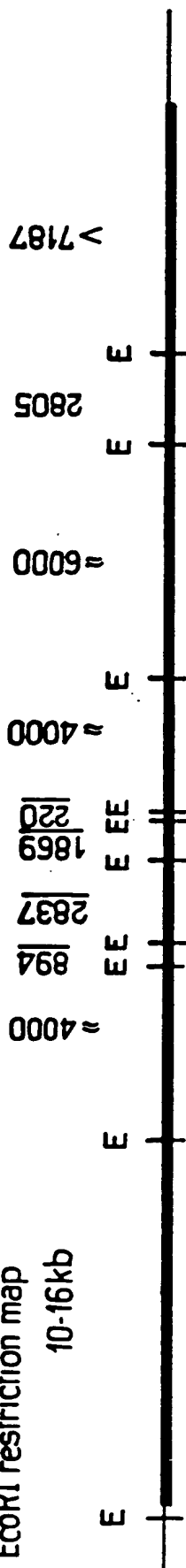
FIG. 1

A) Genomic structure of the nCL1 gene

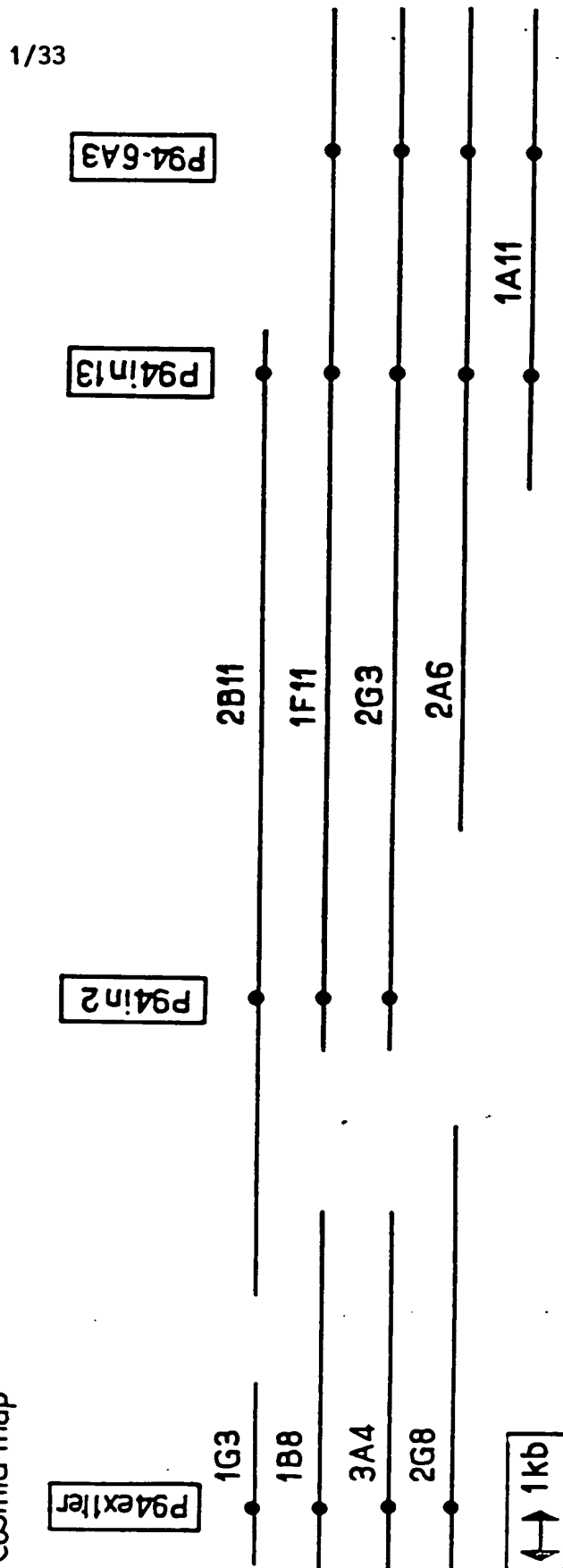


B) EcoRI restriction map

10-16kb



C) Cosmid map



SUBSTITUTE SHEET (RULE 26)

[illegible]

SUBSTITUTE SHEET (RULE 26)

[illegible]

FIG. 2B/2

1330 1350 1370 1390 1410 1430
G T T G C T C T C C G G A G G C T C C G G A A C T T C C A G A T A C T T T C G G A C C A C C T C A G T A C G G T C T G A G G T C C T C G A G G T G A T T T C G A G C T T C
C S A G G C R N F P D T F W T N P Q Y R L K L L E E D D P D D S E V I C S F

1450 . 1470 1510 1530 1550
C T G G T G C C C T G A T G C A G A A C C G G G A G G A C C G G A G T A G G G C C A G T C T C T T C A C C A T T G G T C C C A T C T A C A G G T T C C C A A G A C A T G C A C G G A C A G C A C C A C T G
L V A L M Q K N R R K D R K L G A S L F T I G F A I Y E V P K E M H G N K Q H L

1570 1590 1610 1630 1650 1670
C A G A G C A C T T C T C T G T A C A A G C C T C C A A G C C A G G A G G A A A C C A T A C A T A C G G A G G T G T C C A G C C T C C G C T G C C C A G C A G T A C G T A C T C G T C C C T C C A C C
Q K D F F L Y N A S K A R S K T Y I N M R E V S Q R F R L P P S E Y V I V P S T

1690 1710 1730 1750 1770 1790
T A C G A C C C C A C C A G G A G G G A A T T C A T C C T C C G G T C T T C T G A A A G A G G A A C C T C T C T A G G A A G T T G A A A T A C C A T C T C C G T G G A T C G C C A G T A A A A A A A A A A C C A A G
Y E P H Q E G E F I L R V F S E K R N L S E E V E N T I S V D R P V K K K T K

1810 1830 1850 1870 1890 1910
C C C A T A C T T C G T T C G G A C A G A G C A A C A G G A C T G G T G G A C C A G G A G T C A G A G G G C A A G C C A A C A A G C C T G A T A G C A A A G C A G T C C C C A C A C C A C A G
P I I F V S D R A N S N K E L G V D Q E S E G K G K T S P D K Q K Q S P Q P Q

1930 1950 1970 1990 2010 2030
C C T G C A G C T C T G A T C A G G A A G T A G G A A C A G A C A A T T C C G G A C A T T T C A A G C A G A T A C C A G A C A T G A T G G A C A T C T G T G C A G A T C A G C T C A A G A G G T C C T T A A C A C A G T C
P G S S D Q E S E Q O Q F R N I F K Q I A G D D H E I C A D E L K K V L N T V

2050 2070 2090 2110 2130 2150
G T A C A A C A C A G A C C T G A A C A C A C A C G G T T C A C A C T G C C T G C C G T A G C A T G A T T C G G T C A T G G A T C A G A T G G C T C T G G A A G C T A A C C T T C G A G G A G T T C C A C C A C T C
V N K H K D L K T H G F T L E S C R S H I A L M D T D G S G K L N L Q E F H H L

2170 2190 2210 2230 2250 2270
T G A C A G A T T A G C C T G G C A G A A T T T C A A C A C T A T G A C A C A G A C C A G T C C G G A C C A T C A A C A G T A C A G A T C C G A A T G C A A T G C A G T C A A C C A G C G A C A T T C C A C C T C A A C A G
W N K I K A W Q K I F K H Y D T D Q S G T I N S Y E M R N A V N D A G F H L N W

2290 2310 2330 2350 2370 2390
C A G C T T A T G A C A T T A C C A T C C G G T A C G G A C A C A A C A C A T G A C A T C G A T T T C A G A T T C A T C T G C T T C G T A G C C T G G A G G C A T G T T C A G A G C T T T T C A T G C A T T T G A C
Q L Y D I I T H R Y A D K H M N I D F D S F I C C F V R L E G M F R A F H A F D

2410 2430 2450
A A G A T G G A C A T G G T A T C A T C A A C G T C A A C G T T C T G G A T G G C T C A C C A T G T A T G C C T A
K D G D G I I K L N V L E W L Q L T M Y A

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FIG. 2C

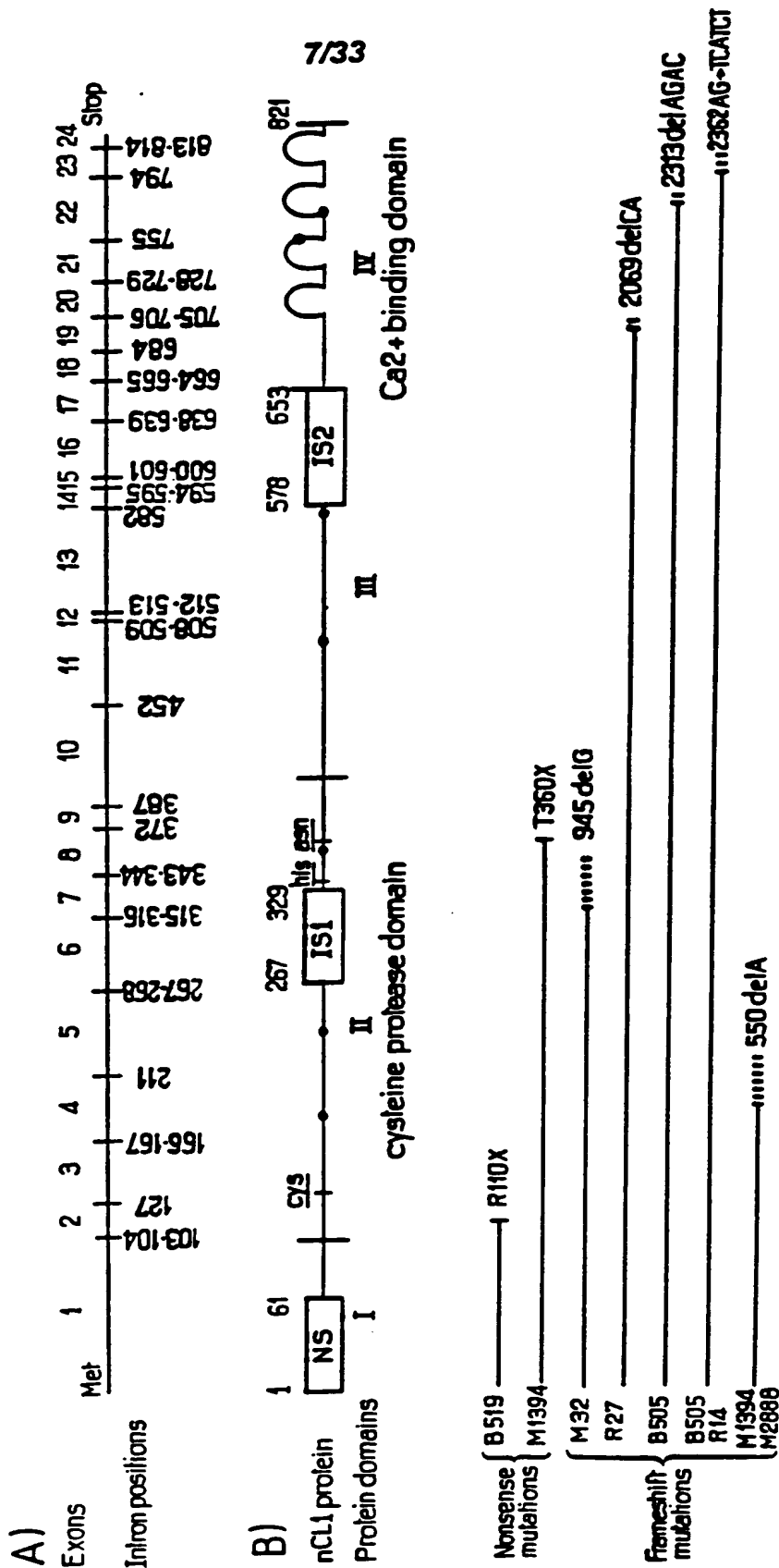
SUBSTITUTE SHEET (RULE 26)

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121 ctcactagtcattgtctctctcatcttacccttaccctaccctcttgatcggctcatgcttagctgacctctctgcaagcaatggatggaaacacccctgtcctcttgcattgt
141 ggaggaaagtgctcgtctgttcgaagcgcctgggtcttgaggagagtgctctgtcagagtgcttacctgctctgagctgagctgctcgcagagcctggacacccctctgtcgt
161 agcctcctcatccctcagctgcctccaccatggcgaggaacacacacagcactgggtcttactgctgtggggctaaactaactcagtggaataggctgggttaccttgggctgcaca
181 acctcaagcttggctgacttctgaaacaaagctgacttgaataggagagcactgagctggctctctgtctctgtctctcaatttagatatcagccatgcatgactgcatggctt
201 ccaatcatatccctcacttccctacaaagagacactgaataggagagcactgaaatctgaaatctgcaattgcaattctcttgagcatagaaatggctcagatgctt
221 ttcccaagacataaaggaaaggaggaagatgcttgcgtcaaaagacatacagataaataaggctcatgtctcttggcaattctcttgagcatagaaatggctcagatgctt
241 tcttagctctctgtcactactgacctgtcgcataagccggcgcaaacacctgaacgcagctgtctgtctcaacctctggacactggcctgcgcatatctataggctacctg
261 tgtttaccacccgttctctctctcctgcctcagcaacggaaaggctggccgtgaaatgcagcagaggttaacgaaagtaaacccgtcaattgtaaaagtaactcaattctctctt
281 gtaattgctctcatctctgtctcacaaggttcacagcttataccaaattgaagaaaggcttcttgcctataaacattttgcagctcaggtgtcactgattctcattctct
301 aatccattatccaatatnaaaatcgaacacaggctgggctcagggcatatctctttaaataagggaagaaatttcaacagcttctctctcttgcacccctctctt
321 cccaattatcttgggtcacctctgaaatttagctgaaatctgggaatgtagtcacagg

Figure 3:

Human	1	MPTVISASVAPRTAAERPSRGPVHPAOSKATEAGGNPSGIYSALISRNFP	50	100
Rat	2PT.....G.T.....H.G.....		
Pig	3			
Cow	4			
	1	EICENPFIIIDGANNRDI	150	200
	2G.....D.....L.....		
	3G.....D.....L.....		
	4G.....D.....L.....		
	1	EICENPFIIIDGANNRDI	150	200
	2G.....D.....L.....		
	3G.....D.....L.....		
	4G.....D.....L.....		
	1	KAYAKLHGS	250	300
	2T.....K.....R.....		
	3T.....K.....R.....		
	4T.....K.....R.....		
	1	DERPRTULIPVOY	350	400
	2V.....E.A.L.....		
	3V.....E.A.L.....		
	4V.....E.A.L.....		
	1	ICNTADALQSDKLOQTWTSVNE	450	500
	2E.....TG.....		
	3E.....TG.....		
	4E.....TG.....		
	1	NKQ	550	600
	2R.....E.....M.....K.....		
	3R.....E.....M.....K.....		
	4R.....E.....M.....K.....		
	1	OESEEGKGTSPDKOKOSPOPOP	650	700
	2D.G.....GE.....R.....HT.....		
	3QD.....EK.....K.E.SNT.....		
	4QD.....EK.....K.E.SNT.....		
	1	NKIKAWOK	750	800
	2H.....S.....		
	3H.....S.....		
	4H.....S.....		

FIG. 4



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FIG. 5

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FIG. 6

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FIG. 7A) EXON 2Normal
sequence

AATCCCCGATTTA



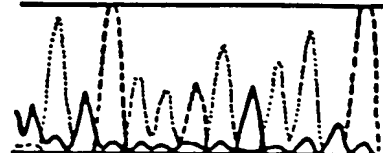
B519

CGA → TGA
Arg110 Stop

AATCCC*GATTTA

B) EXON 8Normal
sequence

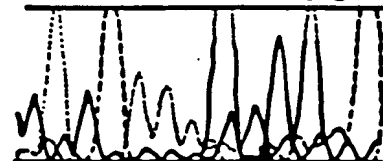
AGCTGGTGCGGCT



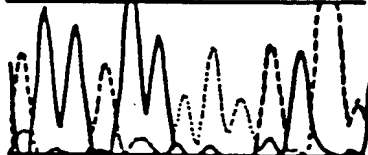
M2407

GTG → GGG
Val354 Gly

AGCTGGG*GCGGCT

C) EXON 13Normal
sequence

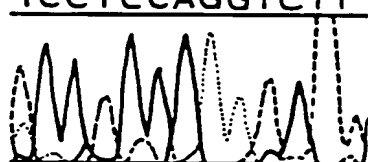
TCCTCCGGGTCTT



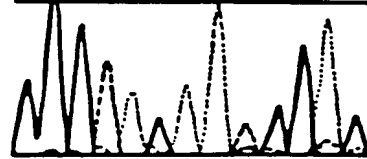
R 12

CGG → CAG
Arg572 Gln

TCCTCC*AGGTCTT

D) EXON 22Normal
sequence

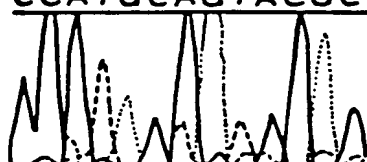
CCATGCGGTACGC



Amish

CGG → CAG
Arg769 Gln

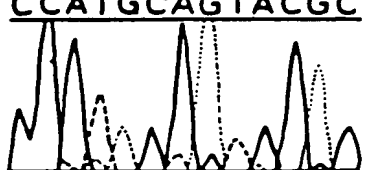
CCATGC*AGTACGC



B501

CGG → CAG
Arg769 Gln

CCATGC*AGTACGC



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LISTE DE SEQUENCES

(1) INFORMATION GENERALE:

(i) DEPOSANT:

- (A) NOM: AFM
- (B) RUE: 13, place de Rungis
- (C) VILLE: PARIS
- (E) PAYS: FRANCE
- (F) CODE POSTAL: 75013
- (G) TELEPHONE: (1) 45 65 13 00

(ii) TITRE DE L' INVENTION: LGMD GENE

(iii) NOMBRE DE SEQUENCES: 4

(iv) FORME LISIBLE PAR ORDINATEUR:

- (A) TYPE DE SUPPORT: Floppy disk
- (B) ORDINATEUR: IBM PC compatible
- (C) SYSTEME D' EXPLOITATION: PC-DOS/MS-DOS
- (D) LOGICIEL: PatentIn Release #1.0, Version #1.25 (OEB)

(2) INFORMATION POUR LA SEQ ID NO: 1:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 3018 paires de bases
- (B) TYPE: acide nucléique
- (C) NOMBRE DE BRINS: double
- (D) CONFIGURATION: linéaire

(ii) TYPE DE MOLECULE: ADN (génomique)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1:

TGATAGGTGC TTGTAACTG TGCTTAACGA AAACATACCG TGTGCTGTAG GGA	60
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CTTACGAGAA CCTATCGATG ATGTTAAGTG AGGATTTTCT CTGCTCAGGT GCACTTTTTT	180
TTTTTTTAA GACGGAGTCT CTTTCTGTCA CCTGGGCTGG AGTGCAGTGG CGTGATCTGG	240
GTTCAACAACA ACCTCTGCCT CCTGGGTTCA AGCAATTCTT CTGTCTCAGC CTCCCAAGTA	300
GCTGGGATTA CAGGCACCCG CCGCCACACC CGGCTTATTT TTGTATTTTT AGTAGAGACA	360
GGGTTTCACT ATTGTTGACC ATGCTGGTCT CGAACTCGTG ACCTCATGTG ATCCACCCGC	420
CTCGGCCTCC CAAAGTGCAG AGATTAGAGA CGTGAGCCAC ATGGCCCAGC AGGACCACTT	480

FIG 8A/1

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TTTAGCAGAT TCAGTCCCAG TGTTCAATTT GTGGATGGGG AGAGACAAGA GGTGCAAGGT 540
 CAAGTGTGCA GGTAGAGACA GGGATTTTCT CAAATGAGGA CTCTGCTGAG TAGCATTTC 600
 CATGCAGACA TTTCCAATGA GCGCTGACCC AAGAACATTC TAAAAAGATA CCAAATCTAA 660
 CATTGAATAA TGTTCTGATA TCCTAAAATT TTAGGACTAA AAATCATGTT CTCTAAAATT 720
 CACAGAATAT TTTTGTAGAA TTCAGTACCT CCCGTTACCC CTAAGTAGCT TTTTGTCAAT 780
 ATTGTTTTCC ATTCATTGA TGGGCAGTAG TTGGGTGGTC TGTATAACTG CCTACTCAAT 840
 AACATGTCAG CAGTTCTCAG CTTCTTTCCA GTGTTACCT TACTCAGATA CTCCCTTTTC 900
 ATTTCTGTC AACACCAGCA CTTATGTCA ACAGAAATGT CCCTAGCCAG GTTCTCTCTC 960
 TACCATGCAG TCTCTTTGC TCTCATACTC ACAGTGTTC TTCACATCTA TTTTAGTTT 1020
 TCCTGGCTCA AGCATCTTCA GGCCACTGAA ACACAACCCT CACTCTCTT CTCTCTCCCT 1080
 CTGGCATGCA TGCTGCTGGT AGGAGACCCC CAAGTCAACA TTGCTTCAGA AATCCTTTAG 1140
 CACTCATTTC TCAGGAGAAC TTATGGCTTC AGAATCACAG CTCGGTTTTT AAGATGGACA 1200
 TAACCTGTCC GACCTTCTGA TGGGCTTCA ACTTTGAACT GGATGTGGAC ACTTTTCTCT 1260
 CAGATGACAG AATTACTCCA ACTTCCCCTT TGCAGTTGCT TCCTTTCCCT GAAGGTAGCT 1320
 GTATCTTATT TCTTTAAAA AGCTTTTTCT TCCAAAGCCA CTGCCATGC CGACCGTCAT 1380
 TAGCGCATCT GTGGCTCCAA GGACAGCGGC TGAGCCCCGG TCCCAGGGC CAGTTCCTCA 1440
 CCCGGCCCAG AGCAAGGCCA CTGAGGCTGG GGGTGGAAAC CCAAGTGGCA TCTATTCAGC 1500
 CATCATCAGC CGCAATTTTC CTATTATCGG AGTGAAAGAG AAGACATTCC AGCAACTTCA 1560
 CAAGAAATGT CTAGAAAAGA AAGTTCTTTA TGTGGACCCT GAGTTCCAC CGGATGAGAC 1620
 CTCTCTCTT TATAGCCAGA AGTTCCCAT CCAGTTCGTC TGCAAGAGAC TCCGGTGAGT 1680
 AGCTTCCTGC TTGCTGGCTG GGTTCCCCC CCACGGAGGA GTCCTCTCAC TCAGCACCTC 1740
 CGGCAGCTCA GCTGTGCACA TGGGCACTGG GGAAGGATC CTGGCAGCAG CTCTGCTGGG 1800
 CTCTGTCTT AAGTGTGAAG CAGGGAGGAG AGGAACAGGT CTCAGATATT TCACCAAATC 1860
 TCAGCAAAAT CCAGAGGGAG AGCGCAGGAG GTGGGTGAT TCTTATGCTC TGGCTCTTC 1920
 TCTCTGAAAA AAAAAAAAAA ATCTTGCTT TTATAAAGT GGGTGGAACT CAGTTTAATT 1980
 CATCCTGTAA AAATAAATAT TCCTTTCTCA GAACAAATTC CAGACAGCCC AGATGTACCT 2040
 GTTCGTTTTA ATATTATTCA TCTTGGTAAG ATTATTTTCA TTTCTCTGGC TAAAATCATG 2100

FIG 8A/2

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ATGTTATTCT TCTTTAATTT ACCAATGGCC ATTCTTTCTG AAACACAGAA ACCCTAGAAA 2160
GAGAAGAGTC ATAGGCAAGG AATTTTTTTC ATGCATAAAA TGTGCGGTT AAAGAGAGAG 2220
AGACCTAGCA ATCGCTTTGG TCCACCTACC TCACCTCATA AGTGAGGAGT CAAGGCACAC 2280
TAGAGTGAAA TATATCTAGT GGGCACATGA CAGAGCCCGG ATTAAAACTT TGTTTTAGGA 2340
AACTCTCCCA GCCTCTGGGT TTCATTTACA GTGATCGCCA GGAGGGAAAT CACATTCCCC 2400
TGGCTCACCT CTCTGATCAT CCCTCCAGTG TGA CTCTTGT TCTTAATTCT AGAAATATTT 2460
ATTGAGCATC TACTAGTGCC AGCACTGGGC AAGCAACTGG GGGGACAGCA GTGAGTAAGA 2520
AAGACCAAAA TTCCAGCTGT CTTGGAACCT AGGGTCCTGA AGGGAAGATG GGCATTGAAC 2580
AAGAGTGACA TTGTCAGGAG ACGATGTTCT GGGTGCCACA GGATCATGTG GCAAGGAGAG 2640
CTAACCTGGT CCAGGGAGAC AAACCCTCTC TGAGGAAATG ATGACAAGCT GAGACCCAAT 2700
ACTATTGATT AGCCATGGTT TTCTTTAACC TAAGGTGGGC CAGGCATGGT GGCTCATGCC 2760
TATAAACCCA GCATTTTGA AGGCCAGGC TGGAGGATTG CTTGAGCCCA AGAGTTAGAG 2820
ACCAGCCTGG GCAACAGGGT GAAAACCTAT CTCTTTTGTA CTAAAAATTC AAAAAATTAT 2880
CCAGGCATGG TGGCACATGC CTGTGGTCCT AGCTACTCAG AGGCTGAGGT GGGAAGATCA 2940
CTTGAACCTG GGGAGTTTGA GGCAGCAGTG AGCCGAGATC ATGCCACTGC ACTCCAGGCT 3000
GGGTGACAGG AGTGAGAC 3018

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(2) INFORMATION POUR LA SEQ ID NO: 2:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 11451 paires de bases
- (B) TYPE: acide nucléique
- (C) NOMBRE DE BRINS: double
- (D) CONFIGURATION: linéaire

(ii) TYPE DE MOLECULE: ADN (génomique)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 2:

GATCCACCCG CCTTGGCCTC CCAAAGTGCT GAGATTACAG GTGTGAGCCA CCACGCCCAG 60
CCGACACTGC CCTAACTCTC AAGTTGCATC CTTACTCGAA TAGTATGACA GTGTGGGAAG 120
CAGCATGGGA CAATGTAAAA AGGAGGCATG TTTCTGGCTT CTGCTACTTA CTAGCTGTGT 180
GTCTTTGCAC GAGTTTCTTA ACCTCTCTGG GCCTCAGTTT CTTATCTGA AAAATAACAA 240
TGATAGTATT CCCTTCACAG GGCCAAATGG AATACTATCA GGAACACTAC ATAATGGAAC 300
TCAATAAATA ATAGCTACTG CGGCCGGGCG CGGTGGCTCA CATCTGTAAT CCCAGCACTT 360
TGGGAGGCCG AGGCGGGTGG ATCACAAGGT CAAGAGATGG AGACCATCCT GGCCAACATG 420
GTGAAACCGT ATCTCTACTA AAGATACAAA AATTAGCTGG GCATGGTGGC GCATGCCTAT 480
AGTCCCAGCT ACTCGAGAGG CTGAGGCAGG AGAATCACTT GAACCCCGGA GGCAGAGGTT 540
TCAGTGAGCC AAGATTGCAC CAGTGCACTG CAGCCTGGCG ACAGAGTGAG ACTCCGTCTC 600
AAAAAATAC CTATCTATCT ATCTGTCTAT CTACTGTTAT TCTTACCTGG TCATTTTCCTT 660
TTTGTTTCAC AGGAAATTG CGAGAATCCC CGATTTATCA TTGATGGAGC CAACAGAACT 720
GACATCTGTC AAGGAGAGCT AGGTAGGAAA GTGCCTCAGG TCAGATCCTG CCAGATGATC 780
AAGGGGTGAT TACAAGGTGT GATCCCCTTC CAGGAGGTAA AGGGACAATC TGTGCTTGCT 840
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CATGACAAAA GCCCTGCTTT TCACTGTATC GTCTTTCTTG GAAGACAGCT CTGTGACTGT 1080
GCACCAAGCA TGCCCCTTGG GCATGGAGAT TCTAGATACA CACACAAAAG GCATCGCCAA 1140
GGAAAGCACT TGTAAGTGA ACCCTTGGTT TAAATTGGCC CAGCATAGCT CCATCTTTAA 1200

FIG. 8/B1

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TCAAGTCTCC CTTGTCACAC TCTCAGGTTG GCATTTTCAC TTAAACCCAT CCTCCCTTAA 1680
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GCAATGTCTT ACTGCCCCCT ATAGACGGGT TCCAGGGCAG CTGCCTACCT GGCCTTCCTT 1920
CCAATACAAA TCATCTTGGT GGATGGTTCT CTGAGGCTCA GTCTTCGCTG AAGTCAGAAG 1980
AGGAATTGGA CTCACATTGC AAAGGCACAG GGCAGGGCAG ATTCCTACA GGTGTTAGGA 2040
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AGTTTATACT GCAGTTGGAG GAACTGCCTG CAGCCTTGAG GAAAATGTCT AGTCACAAGG 2160
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TTGACACCTC TGTAAGGTCA GATCTGGAAG TAGGAGAGTG GGCACCAAGG GAGTCCCCGT 2280
TCAGGGAAGT GGAGTGGCTG GCTGGGATTG GGGCTTTTTT TTCCCAGGAG GAGCAGGAGT 2340
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CTGCCTGACC CTGAACCAGC ACCTTCTTTT CCGAGTCATA CCCCATGATC AAAGTTTCAT 2460
CGAAAACTAC GCAGGGATCT TCCAATTCCA GGTGAGGTAA TGAGAGTGTA GTTAAGAGGG 2520
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CTTCCACCC ATCTACCCGC AGCGGCAACA GTCGGCATGG ACCCCCTTAA GGCTTCAAGC 2640
CTGGGAGGAA GCAGTTGCTT ATCTCTGGCT CCCTAATCCC TCCCCACCA CCTTCCACTA 2700
TGTCCCAGAA AGACAGGAAG ACATCCTGTT TACTGTGGGT CTATTTTGT CTTTGCAGCT 2760
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FIG. 8B/2

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2000-04-27

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AGAGTCTGCT TAACCTGGGG ATCAGGCTTC TTGTTTGCCC TAGAACTGAA TCTGATGGTT	3000
CTAGAATCCA TCCAGCTACT GGAAATTTTC TGGGTCCCAG TCACCTTGGC ATAGAGCTGG	3060
TGCTAGAGCA GAACCAAACCT GAATTCTACC TGTGAGGGTC TCGTAGCTTC CGGGATGCTG	3120
GGGAGTCAGC CTGTCTCCAG CTTCAAAGGC TCCCTCATGT CCCAGGATGA CCCACATTAT	3180
CAGTTCTTGC TCCCCGGGTC TTGCACCTCA GCACGGAAGG CCTCAGAAAA GGTCTGTCTC	3240
CAGGCTCAGA CTCCCCCTCC TGCCGCCTTG GGAACATGGC ATATTTAAAG GGTCTCAGAT	3300
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AGTGCCATTG AAAAGGAGAC TAAACCACAT TTGGCCCTTT TCAGTTCAAA CTGATTCATT	3420
CAAAAAAGAG CGACATCCAA ACTTGAAATG ATTGAACAAT GTTCCTGCTA CAGCTAGAAT	3480
AGATTCTGGG TCACTTTGTT CCTCCGTTTC AATCCTTGTT CTTCAGTTTG GCATCAAGAA	3540
ATACCTAAAT CAGCACAGTG CCTTCACTGC ATAGTTCCCA ATCCTGGCCA CATTGAATCA	3600
GCTGGGGGCA CCTGAGAGTG CTGACACCCA GGCCCTGCCC CAGACCTGCT GAGCAGGAGA	3660
ATGAAAATCT TACATCCTAA GACACTCATG GAGCACCTAC TCTACCCATT ACTGGGCTGG	3720
ACTCTGTGGA AGACATGAAG TATATGTAAC TCACTTCCAG CTCTCAAAAA GCACCCAGTC	3780
CAGTTAGAGA CAGATTTACA CACCCCAAAC ACAAATAGG ATGAACAGGC ACCCAGATGC	3840
AGAGTCCAGG AAATGATGCT GCTTTGGGAT TCAAGAACCC CCTGAGGAAT GTGGAGGAAG	3900
GACACATTTTCTAACAGTAA TTTGAGTATG TGA CTCTGTG CGTGACGCTT CTGTGCAGTT	3960
CTGGCGCTAT GGAGAGTGGG TGGACGTGGT TATAGATGAC TGCCTGCCAA CGTACAACAA	4020
TCAACTGGTT TTCACCAAGT CCAACCACCG CAATGAGTTC TGGAGTGCTC TGCTGGAGAA	4080
GGCTTATGCT AAGTAAGCAA CACTTTAGAA TGTGAGGTGG GGCTAGAGGT GAGAAAGTGG	4140
GTTGCAAAAT CCAGCCGAGA CCTCACTCAC AGGAAGAGGC ATGTGCCTCT ATACGTGCAT	4200
ATGTGTGGGC ATGCAAGTCC AACTGTGACC CAAAGTTAGA GATCAGTTCC AGGCAACAAC	4260
AGCTCTAACT AAAAACATTA AATTTAAGAG TAGAAATGAA GATTTGCATA GAAGACCTTT	4320
AGCTTTAGCT CACCATAGCG AGTTCTTTCA TTGCACCTCC ATGGTGGCAT TGCAAGTCTT	4380
GGGATCAGAG CATGTGCCA GGGTCTCGAT TGGCTCAACC TCATGTGCTT ATAGAAGATT	4440

FIG. 8B/3

SUBSTITUTE SHEET (RULE 26)

17/33

TATAAAGACA TGTTGTCTCT CAACTTAAAA GCTCCACCCC AGATGATAAT AATGGATTTT 4500
CAAATTTTGG AACAAAGGTCA CTCTGTAATG CAGGCTGGAG TGCAGTGGTG CAGTCACGGA 4560
TCACTGTAGA TTGACCTCCT GGGTTCAAGG TGCTCCTCCC ACCTCAGCCT CCCAAGTAGC 4620
TGGGACTACA TCGGGGCATC ACCATGGCCC TTTTATTTTT GTATTTTTTT GTAGAGCGGG 4680
GTTTTCCCAT GTTGACCCAG ACTGTTCTCG AACTCTTGGG CTCATACAAT CCACCAGCCT 4740
TGCCCTCCCG AAGCGCTGGG ATTGCCGGTG TGAGCCACCA CACCGGCAGC TGCTAATGGC 4800
TTTAATGCAG CCCTTCCTCA ACGTTCAGGA TGTAGTGGA AGAGCTCTCA GGAAGTGGGG 4860
ATAGCTGGGT TTCAATCCCA GTGCTTCTGG CTCTCTGTGG TCTTGGGTGG GTCACCTAGC 4920
CTCTTGAGCT CAGTTTCTTC ATTATGAAGA AAGGGAATCA TTGTTTCCAT CCCATGAGCT 4980
CATAGGGTTA ATGTGGAATT GATGAAAGAA CATCACAGCA TCCAAGAGGT AAAGTTCTGG 5040
TGGCAGTGGT ACCTGGGTTT TGTTCCCTGG AACTCTGTGA CCCCAAATTG GTCTTCATCC 5100
TCTCTCTAAG GCTCCATGGT TCCTACGAAG CTCTGAAAGG TGGGAACACC ACAGAGGCCA 5160
TGGAGGACTT CACAGGAGGG GTGGCAGAGT TTTTGAGAT CAGGGATGCT CCTAGTGACA 5220
TGTACAAGAT CATGAAGAAA GCCATCGAGA GAGGCTCCCT CATGGGCTGC TCCATTGATC 5280
TAAGTCTGGG GTGTGGGGCA CAGGGTGGGG AGCTCCAAGT GTCAGGAAGC CTTTACCCA 5340
ATGAAGGGCA GCATAGAGCT TTTGTGTGGG ACAGAGCGAA TGTTTTGTTT GAGGAAGCAG 5400
GAACTGGCTC TCAACTTTGA GGAAGTGGAA TTTCTCAAGG GAGAACAGTT CTTCCGGATT 5460
TTCAATAAAG AACTGGTCA AGGACATTTT AAGCCCTGGA ATGTCAGTGG AAATCAGTCC 5520
AGAGGCCTGT GTCAGTGGAG GCCTCCCTTG CTGGTGCTCC TCAGTCTCAG CACGCTCCCA 5580
TTAAGCTGGC CACGTACTTG GCTGTGGACC TGAGCCCACC ATTTCCCTAA GAAAGCCTCC 5640
CAGTCACTGG GCTTTCACCA CACCTCCCCG CTTGAGACGT GGGCTTTGTG TTGTTACCTG 5700
GGAGAAGCTA AGCCTGCAGC ACCTTTCAGT GCAAAGAAAT GCTGTGAACT GAGACAGGAG 5760
CCAAGGGTAG GGAGATGGCC GCCCATGGCC AGGCCTCCTT CAGGGGGCAT GCCTTCCCTG 5820
AGGGCTGCTC AGTATATTGA TATGATAATC TTAGTGTTTT CCATTGGGGA GGATGGGGCT 5880
GAAGCTGAAT TCCTGCCCCT TCTTCTCCCA ACACGCCCAA TGGACAGCTT GGAAGGTCAG 5940
TTAGCACACA ACACCATGGA TGAACTTTTT TTCTGTATCA CTTTTCTCCG TCTTCTCTCC 6000
ATTCTGTCTC TGTTGATCTC TCCTCTCTCC CTTTGTCTGT CCCATCTCTT TCTCTCTCT 6060

FIG. 8B/4

SUBSTITUTE SHEET (RULE 26)

18/33

CCTTCCCTTT CCACCCTTCT GTGTTTGTTT TCTCCCTCCC CTGTGTTGTT CCCTACATTG 6120
TCCATCGGGC CTCAGGATGG CACGAACATG ACCTATGGAA CCTCTCCTTC TGGTCTGAAC 6180
ATGGGGGAGT TGATTGCACG GATGGTAAGG AATATGGATA ACTCACTGCT CCAGGACTCA 6240
GACCTCGACC CCAGAGGCTC AGATGAAAGA CCGACCCGGG TGTGTACACC TCCGATTATC 6300
AGAACTGACC ATCCCTCCAA CCCACATGAC CCCGCCCTAT TAGTGTGAGA CTCCCCTCAG 6360
CAGCCAGGGC CTTACCCACA CACCCCCACC TGGCACCTCC CAAGGGTCTG GGTGAAATA 6420
ACTTGCTCAG CCAAGGCTCC TGAAGAGGGT GCAAGAACCA GGATTTTGA GGAATCTCT 6480
GCTGGAGTTT CTGCATATTG CATGGTCCAG GCAGTTCCTC TCATAACGAA CTATCAGACA 6540
GAAATACTTG TAAAGATACT TCATTTATTT TGAAATATTT TTCCTCTTCT AATGTATTCA 6600
TTTATTCATT CAACACTTAT TTTTGAGCTC CTACTATGTT CCAGGCACTC CTCTAGCAAA 6660
CAAAGCAAAT TCTCTCCTCT TTTTCAATAT TTGTGGAAAA AGCAAGGTCT CCCTCTTGTA 6720
GAGTTTATAT TCTAGTATTT TCATAAGTTA TACCTGCTCA CTGGAGAATA CTGAGCCATA 6780
CAGAAAAACA CAGAGGAAAA TTTCACCTAT ATTTTCCCC ATGTAAAGAT AACCACCTT 6840
AACATCTAGT ATATGTTCTT CCAGGATTTT TCTATGCACA CACTGAATCT GTATTTTTAT 6900
TTTTAAAATG TTATCATATT GTATGTACCT CTTTGCAGCC TGCTTTTTTC AGTTAGTTTT 6960
TTTGTTTTTT TGGTTTTTTT TTTTTTTTGG AAACCAAGTC TTGCTCTATT CCCTAGGCTG 7020
GAGCACAGTT GTTGCCATCT CGGCTCACTG CAACCTCTGC CTCCAAAGTT AAACCTAATTC 7080
TCCTGCCTCA GCCTCCCGAC ATAGCTGGGA TTACAGGCAC ACACCACCAC ACATGCCTAA 7140
TTTTTGATTT TTTIAGTAGA GACGGGGTTT CACCATGTTG GCTGGAATGG TCTTGAATC 7200
CTGACCTCAA GTGATCCACC TGCCTCAGCC TCCCAAAGTG CTGGGATTAC AAGTGTAAGC 7260
CACCACACCC GGCCTAGTTT GATATTCTTA ATGTGCCCAA AGTATTCTCC TGTAACATTT 7320
TTAATAGCT ACACAATATT CAAACACACA GATATGTTAT AATTATTIA CCAATACCC 7380
TATTATTGGA AAGTTGAGTT CTTTTTTTTT TTTGTTTTGT TTTGTTTTGC TACTATTCTA 7440
AAATGCTATA ACGAACATCC CAATAGATAC ATCTTTGTAT ACATCCATGG TGAATTCAT 7500
AGGACAGATT CCCAGCAGTA GAATTGCTGG GTTGAATGAT ATGCTTAGGG TAATGACAGA 7560
AGAGTCATTT CAAGCAGCTT CCTAGGGTCT TAGAACTTAA GGATTAATGA GTCTTCCCGC 7620
CCCCCTCCAG TCTATTCAGC ATGATCTGGA TCATGAGGAC TGAGATCTGG AAGAGACTGA 7680

FIG. 8B/5

SUBSTITUTE SHEET (RULE 26)

62044-3660

19/33

GATCTGGGAG AGGCTGAGAT ACCAAAAGCC CTGGCTCCAC CCATACCCCT CGCCCTGAAA 7740
ACAGCTCTAG GAATTCGCGG GCCTAGCAAG GCTCCGGGAA GCTCCTTTTA AAGCTGTGAC 7800
GTTAGTAGGC ACATGGACCA TAGAGACCTA TCCAGGGCTC ATGGGACTTT AGTGATCCTG 7860
CCCTTCTCCC AAGGATCCCC CATGGCTGCA ACTTGAAAT TTCTGCAAAT GGAAGAGCTA 7920
CTCCTTAGGC ACGGTCATGT CTGAGCAGGG ATCTCCTCGG GCTTTCTTAG AATTCTCTCC 7980
CTGGGCACTG GGACTCTTGA TTTCTTGAAT ATTATGTTCC AGGTGGGTGT GGAGGAGGTG 8040
AGGGGATGTA AAGAAGGCTA GACTTGCCA GCGCAGTGG CTCATGCCTG TAATCCCAGC 8100
ACTTTGGGAG GCTGAGGCGG GTGGATCACC TGAGGTCAGG AGTTCGAGAC CAGCCTGGCT 8160
AACATGGTGA AACCCCGTTT CTAATAAAAA TACAAAAAAT TAGCTGAGCA TGGTGGCAGC 8220
TGCCTGTAAT CCCAGCTACT CGGGAGGCTG AGGCAGGAGT ATCGCTGGAA CACGGGAGGC 8280
AGAGATTGCA GTGACCCGAG ATCGCGCCAC TGCCTCCAG CCTGGGCGAC ACAGCAAGAC 8340
TCTGTCTCAA AAAACAAAAA AGAAAGAAAA AAAGGAAAAG CTAAGACTTA CATGTGTCAC 8400
TTAACCCTT TTCTCAAACC TCTTCTCTT CCAGGAATAG TCAACCCTG GATGGCTTCA 8460
GGGAAGGGG GATCCTGAAG CCCAGGGCAG CCTCCAACCTC TACCCTTCC TCCTTTGAAG 8520
GATACTAAGG GGTCCAGAAA GGAGGGGCAG GACTGTGTTA CCCACCCAC ATCCCAGCAT 8580
CCACATTGCT CTCTGATGGT CAGGACAGAG CTTTCTCAGG GAGACCAGCC TGTCTGGAGC 8640
TGTGTCTCTT GGCCTCTTA AAGGGCCACT GAAGGTCCGT TCGTGGTCGT GAGGCACACT 8700
TTCAGGGAGC AGAGTGGTCT GTGTCTTCAC AGAGCCCGGA AAATGAACTA GTATGAACTT 8760
TGCCTCCAAG CAGCAGAACT TCTGTTCCTC CGCCCTAAT GGGTCTCTG GTTACTGCTC 8820
TACAGACAAT CATTCCGGTT CAGTATGAGA CAAGAATGGC CTGCGGGCTG GTCAGAGGTC 8880
ACGCCTACTC TGTACGGGG CTGGATGAGG TAAGCCTGGT GGGGCTTGGT GGGGCAAGGG 8940
CACCTCCTG GGTAAACCTC ATGAAGTCAG GACTTAGCTG TTGGGGCCCC TGCCCTGTCT 9000
GCAGAGCTTG CCTCCAATCA GGACATTCAG TTCAAGGTCC AAGCCACGCC TGGGAGCAGA 9060
GGGGCCTGTG AAAGTGGTAG AGGTGGATCC TGCCACAGTT GGTGCACAGT TTATCTTTGC 9120
TTTTCGTGCT AAAGATGGCA ATTTTCCAA CATTTCAT ATGACAAATTG AAATATCACT 9180
TAACTTTGCT TTTACAAAGT TGGTTTCATG TGTTCTTGAG CTTCTGTTC TCTCGTGTTT 9240
AGATAGCTAC AGTTGTCTCT GGGTAGCCAC GGGGACTGGT TCCAGAAGCC CCAACAGTAA 9300

FIG. 8B/6

SUBSTITUTE SHEET (RULE 26)

20/33

CAAAATCTGC AGATGCTCAA GTCCCTTCTG TAAATGGAG TAGTATTTGC ATATAACCTA 9360
TGCACATCCT CCCATATACT TTAAGTCATC TCTGGATTAC TTACGATACC TAACACAATG 9420
GAAATGCTAT GTAAATAGTT ATTGCACTGC ATTGGGTTTT TTTGGTATTA TTTTCTGTTG 9480
TTGTATTATT ATTTTTTCTT TTTTGAATA TTTTGATCC ACAATTGGTT ATATGCCAAA 9540
GCCATGGATA CGAGAGGCTG ACTGTTCTGT TTTGCTCCTT CTGGGACTTC TGGGTTTTCC 9600
TGGACCATGT CTGAGACAGG AACGTTGTAA GACCTGTTGC ACACAGTTGG GCAGGTTGTG 9660
CCCTGTACAG AGGGATGGGC TGAGAGGGGC AGTTGCCTGC ATCACCATT GCAGCAGACT 9720
GGAGGGAGTC TGCTTGTTG TAGTTCCTCA GTCAGCAGGG GCCTTTTGTC TTTCTTCCT 9780
TTCCTTTTTT TTTTTTTTG AGACGGAGTC TCACTCTGTT GCCCAGGCTG GAGTGTAGTG 9840
GCACAGTCTC GGCTCACTGC AATGTCCGCC TCCTGGATTG AAGCGATTTT CCTGCCTCAG 9900
CCTCCTGAGT AGCTGGGATT ACAGGCGCGT GTCACCATGC CCAGCTAATT TTTGTATTTT 9960
TAGTAGAGAT GGGGGTTTCT CCATGTTGAT CAGGCTGGTC TCGAACTCCT GACCTCGTGA 10020
TCCGCCCACC TCGGCCTCTC AAAGTGCTGG GATTACAGGC GTGAGCCACC ACGCCTGGCC 10080
AGCAGGGGCC TTTTTTCTAA TTTATATGAA GACACCTAAT TTATATGTGT TAGCAAAGCC 10140
CTCCTGTTTA TGCCTCACCT CCTCCCCGA AGCTCATACG GCAGGATGTT CCTGAGAAAA 10200
TTGCCTCTTA GAAGATAGAG AGGAGATGCC AAGCCTAAGT TAGGCAGACT CAGGAGGATA 10260
GGTCTGACCC ACCCCTGCC ATTCCCCAGC ACACTTGTGA TTAATCTCCT TGGCCAGAGC 10320
CAGGCAGAAC ACCCTCGCGT AAGAGATTTG CCCCCAGCC CCGTCCCAGC CCTCAGCTAG 10380
ACAGAAGATT CCCTTTCCAG AGAGGCTGCA GAGCATGAGA GCTCTTCTG TGTGCTTAAG 10440
GTCCCGTTCA AAGGTGAGAA AGTGAAGCTG GTGCGGCTGC GGAATCCGTG GGGCCAGGTG 10500
GAGTGGAACG GTTCTTGGAG TGATAGGTAG GTGAGGGGAC CCCACGGGAT TGGCGGTGGC 10560
GGGGAACAGG GTCCGGGACA AGGCTGTGTT GGGAAGTGA CCATGAGAGT ATTGAAGATG 10620
CTTGGTATAA AATCACCCTC AAAACCAATG ATCCGCAGAG AAGAGGGGCA CAGGTGTTGG 10680
CTCCAGGGAA GGGCCAGGAG TGAAGCGGG GTGCTGGGGA CCCAGAGAGG TTGCTGACAA 10740
CCATTGGCTG GAAAGGAAGG ATTCCAGAAA GCGTGGGGA GGTCCAGGCA GGAAAAGCGT 10800
ATGAATGCAG GGTCTGGGC TAGAGAAAGT ACTTCCCTTC TTGGGGTCTT GTGTTGCCTT 10860
TCCTGTGAAA TGGGAACAGT ATTATTAGCA CTTACCTTGT GGGCTGATAT TGAGGAGTAA 10920

FIG.8B/7

SUBSTITUTE SHEET (RULE 26)

5334-0700

21/33

CTGGGACTTG	TTTTTGGGCA	AGTGCTGAGC	CATTGCTAAG	ATTCCCCTTA	CCCGTGCTTG	10980
TCCCTTGTAT	TAAGGCACAA	GGGCCCTTTG	AAAAGAATT	TACCTGCTTT	ATCAATTGAA	11040
AGGGATTAAG	ACCTTGGGGG	CCAACCCAAA	ATAAACATGC	GAAGTTATTA	TTTATAGGCT	11100
CCATGCACAC	TTCGTAAAAC	CTCCATGGTC	CTACTGGTTC	CTGATTACCT	CCACTCAATG	11160
AGAGGCAATT	CATTACTGAA	TGAGCCATAA	GCGCCTCTTA	TTTCGAGAGG	GGGATGGCAG	11220
GACTCAGTCG	AGGAGAAGGA	CCGCACCCAG	GCAGCCTGGG	CCCCTCGGCT	CCTGTACTTA	11280
TTTACTGCTG	GGTACTTCCT	AGCCCAGCAT	GTAATTACTG	GTTTCGTTAG	TCATTGTTTT	11340
AGTAAATGTT	TCTTGGGCAC	CTACTACATA	GGAGGCACAG	GTCAAGGCAC	TGGGGATATT	11400
CTTTCTACCC	ACCCCTCCC	TCCCTACACT	GTGATTAGGG	ACTGACCGAT	C	11451

22/33

(2) INFORMATION POUR LA SEQ ID NO: 3:

(i) CARACTERISTIQUES DE LA SEQUENCE:

(A) LONGUEUR: 1834 paires de bases

(B) TYPE: acide nucléique

(C) NOMBRE DE BRINS: double

(D) CONFIGURATION: linéaire

(ii) TYPE DE MOLECULE: ADN (génomique)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 3:

ATTTTTTTTT TTTTTTTTGA GACGGAGTCT CACTCTGCCA CCCAGGCTGG AGTGCAATGG 60
CGCGATCTTG GCTCACTGCA ACCTCCGCCT CCCGGGTTCA AGTGATTCTT CTGCCTTAGC 120
CTCCTGAGTA GCTGAGACTA TAGGTGCCCC CCACCAGGCC CAGCTAATTT TTGTATTTTT 180
ATTAGGACGG GGTTTCACCA TATTGGCCAG GCTGGTCTCG AAATCCTGAC CTTGTGATCC 240
GCCCACCTCG GCCTCCCAA GTGCTGGGAT TACAGGTGTG AGCCATTGCG AGCAGCCCAG 300
AACTCAATTC TTAACCTTTA AAGTATGATG AGAAGAAGGA TCAAGCCCTC ACCAGCCCAT 360
TTAAGGAGTT TAGGCTCAGT CTTGAGGATG TGAGAAGTCA TTGCTATTGG GTTTCACACT 420
GAGGTTAACA GGTGAAGTCA GCATTTTGGT AGTTCACAGC AGCTGCAACT CTTTGTATTT 480
CTCTGATACC TCCTGTCCCA ACCTACATCA GGCCTTCCCT TCTTCCTGCT TCCTTAATTC 540
CTCCATTTTC CCACCAGATG GAAGGACTGG AGCTTTGTGG ACAAAGATGA GAAGGCCCCGT 600
CTGCAGCACC AGGTCACTGA GGATGGAGAG TTCTGGTGAG TCCAGAACCC AGGAAGACCC 660
AGAAGGGTAA GGGTGGGGAA GAGAGGGGAA ATCTCAGACC TCAGTCCCCA GCTAAGGTTA 720
TCAGATTCCA GCCCTTGGGA GATCTTGGCT GTGTTCTCCT CCAGCCCAAG GCCCAGCAAG 780
GATGAGGTTT TGAGAGGAGC CTTCCAGGCC ACAGGGACAA TGAGCCCAGG ACCAGGCCAA 840
CATGACATGG CTCTTGCTC CTGTGTGCCC CTCCGCCACA CACTCTATTC CAGCCACAGG 900
CACCTTGGCC TTAGCACAAT TCTTTTCTGA GCCTAGGAAG CTCCACTTAC CCTGATCTTC 960
CAACGTCAAC CTCACCCTCT CTCAGGTTGT TTCTATTAG GCTTCAAGTC TCAGCTTAAG 1020
GAGAATTTTC AAGTCTCAGC TTAAGGAGAG CCCCCTAAGT TCCCCGAGGA CTGGGATTAA 1080
TTTATGATGC TCATCACCCT TAAAATTGTT TGCTTAAGCC GGGCGCGGTG GCTCACGCCT 1140
GTAATCCCAG CACTTTGGGA GGCCGAGGTG AACGGATCAC GAGGTCAGGA GATCGAGAAC 1200

FIG. 8C/1

SUBSTITUTE SHEET (RULE 26)

08/836734-070297

23/33

ATCTTGGCTA ACACGGTGAA ACCCTGTCTG TACTAAAAAT ACACAAAAAA AGTAGCCGGG	1260
CGTGGCAGCG TCGCCTGTA GTCCTAGCTG CTGGGGAGGC TGAGGCAGGA GAATCACTTG	1320
AACCTGGGAG GCAGAGGTTA CAGTGAGCCC AGATTGCGCC ACTGCACTCC AGCCTGGGCG	1380
ACAAGAGAGA CTCTGTCTTG GAAAAAAAAA AAAAAATGTG GTCTTAGTTT AATGTCAAGG	1440
GAAAGGTTTT GGGTGTTTTT ATTACTTTAT TTTTATTTA AAAACTATAA TAGAGACGGG	1500
CCTCGCTATA TTTCTCGGGC TGGTCTCAA CTCCTGGGCT CAAGCGGTCC TCCACCTTG	1560
GCCTCCCAA ATGCTGGCAT GTGGGCCTGG TCAACATATG GGACCCCAAC TCTACAAAAA	1620
ATTTTAAAAT TAGCCAGATG TGGTGGCGTG TGCCTGTAGT CCCAGCTACT TGGGAGGCTG	1680
AAGCAGGGGG TCACTTGAGC CCAGGAGGTT GAGGCTGCAG TGAAGTATGA TTGTCGTTCA	1740
CTTTTCTTCT GAACGTGAGA TTAAGTGTAG TCAGCAATTT GGCTTAGGAT TATTTATTCA	1800
GAATTTTAA CCGTCACGTT GCGGCAAACC AGGT	1834

FIG. 8C/2

SUBSTITUTE SHEET (RULE 26)

462040-429888

24/33

(2) INFORMATION POUR LA SEQ ID NO: 4:

(i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 14664 paires de bases
- (B) TYPE: acide nucléique
- (C) NOMBRE DE BRINS: double
- (D) CONFIGURATION: linéaire

(ii) TYPE DE MOLECULE: ADN (génomique)

(xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 4:

AGGAGGTGGA GGTTCAGTG AGCCAAGATC ATGCCACTGC ACTCTAGCCT GGGCAACAGA	60
GCGAGACTCT GTCTCAAAA ATACACACAC ACACACACAC ACACACACAC ACACACACAC	120
ACACACATAT ATATACACAC ATATATATAC ACACACATAT ACACACACAC ACGTCTGTAT	180
ATATATGTGT GTGTGTATAT ATACACACAC ACACTATTCT ATATATTCTT GTAGAGCTAT	240
GTGTGTCTCC TGTGCTATTG AGCATGAGCC CTTTTTTTTT TTTTTTTTTT TTGAGACAGA	300
GTCTCACTTT GTCGCCCAGG CTGGCATACA ATGGCGCAAT ATCGGCTCAC TGCAACCTCC	360
GCCTCCTGGG TTCAAGTGAT TCTCCTGCCT CAGCCTCCCA AGTAACTAGG ATTACAAGTC	420
CCCGCCATAA TGCTCAGCTA ATTTTTGTAT TTTCAGTAGA GATGGGGTTT CACCATGTTG	480
GCCAAGCTGG TCTCAAATC CTAGCCTCAG GTGATCCACC TGCCTCAGCC TCCCAAAGTG	540
CTGGGATTAC AGGCATGAGC CACAGCACCC TGGTGAGCAC TAGAGCTTAT TTCTTCTATC	600
TAAGTGTATT TTTGTATCCA TTAGCCACCC TCTTTTCATC CTCCCCTCTC CTCCCTTCC	660
CAGCCTCTGG TAACCACTGT CTGCTCTCTA CTTCCATGAC ATATGCTTTG TTTAGCTCT	720
CACATATGAG TGAGAGCATG CGACATTTAT CTTTCTGGCC CTGGCACATT TTTGAATCAT	780
TGTTAGAAAA GATGATGGTT TGGAGTAGAT ACATCAGAAG TGACAGCGTT TGCCCTAAAA	840
AGGAAAGACA GGCTCCTCTG GGACCCTGAC CAAGTTCCTG TGAATATTT TATTATTGTG	900
CTGTGTTAGT CCTGGGGTCT TCCGTTCCCA GCCCTCCTCA CCTGCTCCCA TATGGCTCTC	960
TCTCTTCTTC CAACCTCTCA GGATGTCCTA TGAGGATTTT ATCTACCATT TCACAAAGTT	1020
GGAGATCTGC AACCTCACGG CCGATGCTCT GCAGTCTGAC AAGCTTCAGA CCTGGACAGT	1080
GTCTGTGAAC GAGGGCCGCT GGGTACGGGG TTGCTCTGCC GGAGGCTGCC GCAACTTCCC	1140
AGGTGGGAGA TGCTCTTGAT GGGGGGAGGG TCTAAGCCGA AAAAGTTCCA GGCAGAAGAA	1200

FIG. 8D/1

SUBSTITUTE SHEET (RULE 26)

152000-41-195000

25/33

GCCTAACTAG TGCTTATTAA GTCTCTCTGT TCCAGACGTC CACTATCTTA TTAAACCTTC 1260
CCTGTTTTAC TGAGAAGGAA ACCACCATGC TGAGAAGTTT GCAATAGGGA GCTGGGTAGC 1320
AACTTTGGAA GCAGGAACTT GTGGGAACAA TGCAGATGCT GCTTGGACTT ACGATGAGGT 1380
TATGTCCAGA TAAGCCCATC CATCTTTTGA AAATACCCTA AGTGAAAAGT GCATCCAATA 1440
TGCCTAACCC CCCAAACCTC ATAGCTTACC CTGGCCTACC CTCAAACATT GCTCGGAACC 1500
CTTGACCTTA AGCCTAAAGT TGGGCCAAAT CATCTAACTC CAAAGCCTAT TTTACAAAGA 1560
AAGTTGTTGT AATATCTCCA TGTAACCTAC TTAATACTTG TACCTAAAAA GTGAAAAACA 1620
AGAATGGTTG TACGGGTACT CGAAATCCAG TTTCTACTGA ATGTGCATCT CTTTCACATT 1680
GTAAAGTTAA AAAATTGTAG CCGAACCATC CTAAGTCAGG GACTGTGAGT ACTGTGTCAG 1740
TAACAGTAAG GGCCTATTG GAGAACCAAG TTAGCAGCTG CTGCAATAGT TCAAGTCAGA 1800
GATGATGAAA ACCTAGACCA AGTCAGTAGC AGCAGAGATG GAGGGGAGAC AGCAGATTTA 1860
GGGAGAGCAT ATTGGGTGAT GTAGGGAAGG AAGAAGAATG ATGTCAAGAT TCCCAGTTGG 1920
GGACCTGACA ACATTGCAAC ATAAGACACA CAAGAAGATC GGGTGGGTGG CTCATGCCTA 1980
TAATCCCAGC ACTTTGGGAG GCAGAGCCAG GAGGATCACT TGAGCCCAGG AGTTCAAGAC 2040
CAGCACAGGC AACATAGTGA CACCTCATCG TTACCCAAAA TAAAAAATAA AATGAGGTGG 2100
GAGGATTGCT TGAGCTCGGG AGGTTGAGGC TACAATAAAC TGTGATCATG CCACTGCACT 2160
CCTGCCTGGG TGACAGAGTG AGACCCTGCC TCAAAAAAAA AAGACACACA AGAGAAAAAT 2220
ATCAGCGTGT TGTTTGTITT TGGTGGAGTT AATTGTGGGG TTCTAGGGAA AGGAATTTAG 2280
CTTGGGACAT GGAAAGTTTG AGGTTCTGT AGAGTGTCCT AGTGAAGATT TGTAATAGAG 2340
CATCGGATGC GCATATTAGA TGGCACTTGG TGATATGATA AGAACTCAA AAATATTTGA 2400
GGAATAAAGG AAAGAAGAGG CCAGACGTGG TGGCTTATGC CTGTAATCCC AGCACTTTGG 2460
GAGGCTGAGG CAGGCGGATC ACTTGTGGTC AGGAGTTCGA GACCAGCTTG GCTAACATGG 2520
TGAAAACCCA TCTCTACTAA AGATACAAAA ATTAACCGGG GATGATGGTG GGTGCCTGTA 2580
ATCCCAGCTA CTTGGGAGGC TCAGTCAGAA GAATCGCTTG AACCCAGGAG GCGGAGGCTG 2640
CAGTGAGCCG AGATCGCGCC ACTGCACTCT AGCCTGGGCA ACAGAGCCAG ACTCCGTCTC 2700
AAAAAAAAA AAGTGAGAGA GATTGAGGCT GGGATATATG GCTCAGGCAT CATGCGCGTG 2760
TAGGGGGCAG TAAAAAGCA GAAGTAAGAA AGATTGCCTA GGGAGGCAGG AAGGGTGAGG 2820

FIG. 8D/2

SUBSTITUTE SHEET (RULE 26)

0036734-0000

26/33

TGAGAGGAGA AGAGGCCCGAG GACCAGATTG TAGTCACCAA CAGCGTTTAA GGGGCAGGTA	2880
AGGAAAACAA AACCATCAGC AAAGACTGAG AATGAAAGCC CAGAGAGGAA GGAAAAGCCA	2940
CACATACAAT CAGTACAGCT CCATCTGAAT AAAGGTAGCG CCCCCCCCCC CCCAAATCAT	3000
TAGAGAAATG CCTGATTGCG TTTTCTGTGG ATTTTTCCTA AGAACCTAGA TGTGGGGAAT	3060
AGAAATAAAT GGTTCCTCT GTCTCATCCC CTCCTGCCC TCTGAGAGGA AGCTGTGATT	3120
GCGTGCTCCC TTTCTGGGGG TGCAGATACT TTCTGGACCA ACCCTCAGTA CCGTCCGAAG	3180
CTCCTGGAGG AGGACGATGA CCCTGATGAC TCGGAGGTGA TTTGCAGCTT CCTGGTGGCC	3240
CTGATGCAGA AGAACCGGCG GAAGGACCGG AAGCTAGGGG CCAGTCTCTT CACCATTGCC	3300
TTGCCATCT ACGAGGTGTG TAGTCCTGAT TGGCTCCAGC CCAGGAAACA TACTTTCCCA	3360
GAGAGGACGC TTCCAGGGGC TTCTAGAGGG GCCCTCTGCT TCCTCAATAC CAGTGACCCA	3420
CAGAGCTCCT GGTATCAGGA CCACTTGTGT TTGTAACAAG CAAAAAATAC CAGGGGGGGC	3480
ATTAGAGAGG CAGTGGAGCG GGCCTGGCAG AACAGGTGCC TGGGGGTCAG GCTTCCGCAT	3540
GCGGGCTGCA GTTGCTGGCA TTGCCTTCCG CAGGCTCCTC ATCCTCATTG ACATCTGAAG	3600
CATCTTCCTT TCTGTTTCTT CTCAAGGTTT CCAAAGAGGT ATAGCAGCAG CAGCGGCCAG	3660
CAGTTGTGTG CAGCACTACC CAGGGGGGGC CGACTCTGTC TGTGGCTCGT CGAGAAGCTT	3720
CCTGGTGGGG TTTGTGGCA GGAATTGTGA TAGGAGAGGG CTTGCCTGT TGTATTTC	3780
CACTTGCAGA GCAGGTGCG TCAGGGCATT GCATGACCCA TGACTACCAC CCCAGGATG	3840
TGCACTTTCT CCCTCGCACC AGACACTGCA CGTCACACAC ATGCCTTTGC AACTCACCC	3900
TCCTCCACGC TTACAGCCAC ACACACAGTC ACACAGACGC GTTCTGAGGG TGGCTGCCCG	3960
CTTGGGATGG AGGAATCACT TCCCTCAGAA CCCAGCCAAG TCCTCTAGGC CTCCTTGGGG	4020
GTCTTCCAG CCTGAGGGGC TTCGGAGCTG AGGACAGCTG TTCTGGTAAG TGTCCCTGAG	4080
TGTGGGGATG ACACATTTC ATTCACTCTG AATCACAACA GAAAAGGGAA GAGGAATTGA	4140
GGTAGGGAGC CTATTTAACC CTGGGAGTC GGGAAGTAGG GAGGTTGAAA CTGTGACATG	4200
GGTGACCAGG GAGTTGGGAA GGGACCCTTG GAGGTGGCTG TGGCAGGACA GGACGTTCTT	4260
CCCAGGGGGC TCATGTGCCC TGGGCTCTCC CCATCTCTCA GATGCACGGG AACAAAGCAGC	4320
ACCTGCAGAA GGAATTCTTC CTGTACAACG CCTCCAAGGC CAGGAGCAAA ACCTACATCA	4380
ACATGCGGGA GGTGTCCCAG CGCTTCCGCC TGCCTCCCAG CGAGTACGTC ATCGTGCCCT	4440

FIG. 8D/3

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CCACCTACGA GCCCCACCAG GAGGGGGAAT TCATCCTCCG GGTCTTCTCT GAAAAGAGGA 4500
 ACCTCTCTGA GTGAGTGCTG GCCCAGCTTT CCCACGTGTT TCTAAAAGCT CACATGGCCC 4560
 ACTCCAGAGG TTGAAGGCAT GAGGCAGCTA GACACGTCTC CTCCAGGGTC CTTCTGCTGC 4620
 TCCTGAGCCA CTGGCCACAT TACCCCCATT CATTCAATTCA TCCATTCTGT GATATTTATT 4680
 GAGCACCTAC TATGTTCCAG GCACTGTCCT AGGCACTAAG GATAGAGTAG TGAAGTAAAC 4740
 AGAAAGAAAT CCCTGCCTTC ATGGAGCTTA ATATTCTAAC ATGAGACAAT AATGGATAGG 4800
 AAAACATAT GTAGCATGTT AGATTTGGAG AGGTGATATG GAGCAAAAAT AAAGTAGGGA 4860
 AGAGGGATAG GAGGTGTTGG GGATGCTTGA AATTTTAGGT TAGCATGGCC AGGAAAGCCA 4920
 CATCCTGTCC CTGGCCACCA CAGATGAGCT CATAGCCCCT GCCACTCTGA TCTCTGTCCT 4980
 TGGAAGATGC ACCAGGTCCA TGGGTAGGTG GCTGGGTCAT GCCTTTGGGG GGCTCTGAGC 5040
 AATACTAACA AGAACCTGCG TGCCTGGGCT TGGCTGTCGG GGATGGTGCT GACATGGGGC 5100
 TGGTTCCTGG GGTGTTGGGTG TTCCAGGGGT TCTCTAGAGG CTGGTTCCTG CTTGGCTGCC 5160
 AGGAAGCCGT GCACCAGAGC AAACCGTCCA CGGGCCTCCT GCTTGCTTCT GGTGACACTG 5220
 AGACCCCA TGTCTGTATT CCTCACAGGG AAGTTGAAAA TACCATCTCC GTGGATCGGC 5280
 CAGTGGTGAG TGGTTTAGAT CTTCTGTGCG AAAAGTCCAG AGGGTCCCCT TCCCTGACCA 5340
 TGCAGGGGAC AGATGGTGCA GGGGAGAATG GGCAGTGGCA GAGGGAATGG GAGTCTGGGC 5400
 TGTGCTGAGC AGTCCCTCCT TGGCACTGCA AATCCTACTT TGGCATGGCC AGAAGTAATC 5460
 GGCCTTAAGC ACCGGGGGCC ATTGAGGCAG TTCAGGGGCT GGGAAATATG GAAGAGGGTC 5520
 CTGGAAGGA GAAGCAATTT GAACAATCGG AGGGAACAAG GCCACAGGAA GGGATGACAA 5580
 GAGCCGCAGC GAACACTGGA TTCTGAGACT GGATAACATT GGATTTTACA CATAGAGAAA 5640
 AGAAAGTAAG CTGGTGCCGG ACCTGGTGTT GACACTTGGA TCCTCCACTT ACCAGCGGGG 5700
 TGACCTGGAC AATTTCTGTA ATCCCTCTCA CTCAGTTTCC TACTCAGTAA AACGGGGATG 5760
 ATAATGTGCC TTGCAAGGCT TTTGTGAGGC TTCATCAATG AGGTGATGTA TGTGAAGTGT 5820
 CTGGCACAGC ATGGGCACTC AAACAGAGGT GCTTTTTCAC ACTTTACACC TTACAAGGTA 5880
 CTTTTCACAT GTGTCATCGC GATACTTGCA AGGTTGCTGA GAGGTAGATG GGGTTATAAT 5940
 CCCTGGTGTT CAAGAAAGGA AGCAGAGGCT CAATGGGGTT GAATGACTTC TCTGAGTTCA 6000
 CAGAGCTCAG TAAGTGGCAG GGTGTTGGAAC TCACATTCAG ACTCTCTGAC TCCAGACTTA 6060

FIG. 8D/4

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GGTTTTTCCG CACCTCCACG CTGAGGCCAG CCCAGGCAG TGAGAAGCCC AAAGTCCGAA 6120
GCACAGAGTG CTGTGTGTTG GGCTCTGTGT GTTGAGGAGT CTTGTGACTG CCTTGGGGCT 6180
TTGGGCTGTA GTCAGCTGAC AGTCCTTTGT GCTCTGTGGG GATGACGTAG GCCAATGGGA 6240
GGACAAATGC CCCTCTGAAC TGTCTTCTGG GCAGTGACAG TCATGGTCAT AATCCTGACC 6300
CTGAGCCAGT GCCAGGTCTC CAAGTGCCTT CTGAATGACC ACAGGCGATT GGTTTTAGTG 6360
GTAGGTGCGT GGGGATCTGT TCTGGTCATC TGGATGCTGG TCATCGGGTG CAGTATTGAT 6420
CAGGACCTGC AAACCCAAAA GCTTATGGGA GCTGGCACGT CACGTGAGTA GAGCAGGCAG 6480
GTGCAGGGTT TTTGATGTCC CTGCACTGAC ACAGTTGTCT GCAGTTCTCC AATTTGACAT 6540
TTGGGCTCCA GTGTCGAGGG TCAAACAAGG AATTTTGGGG CGTGGGCCAA ATCTGGGAAG 6600
ACACAGGGAG CAGGGCCCTT TGGCTCAAGC TGATAGTTGC CGCAGGGATT ACCAGGCCCA 6660
GGGCAGCCTG CCACAAGCTG GGGCTTTTAC CAAAGAAAAT CTCCCTATGT TAAATGCTTG 6720
CTCAAAAATT TTTAAAAAAT ATTCTGTAAG TCAAAATCCA TTGTTAGGTC AGTTTGAGAG 6780
AGCCATGTTT TTGGTGTTTT AGTAACCAAT TTCATTTTTT TATTATTIAT TTATTTGTTT 6840
ATTTTTGAGA CGGAGTTTCA CTCTTGTCAC CCAGGCTGGA GTGCAATGGC ATGATCTCAG 6900
CTCACTGCAA CCTCCGCCTC CCGGGTTCAA GCAATTCTCC TGCCTCAGCC TCCTGAGTAG 6960
CTGAGATTAC AGGTGCCCAC CATCAGCCTT GGATAATTTT TGTATTTTTT AGTCGAGATG 7020
GGGTTTCACC ATGTTGGCCA GGATAGTCCT GAACTACTGA CCTCAGATAA TCCGCCACC 7080
TCAGCCTCCC AAAGTGCTGG GATTACAGGC ATGAGCCAGC ACGCCCGGCC ACCAATTICA 7140
TTTTTTAAAA AAGGAAGAAA GAAAACCTTA GCCAGAAGAT CTTTTTCCTT GCCATATGCA 7200
GTAAGAGTAG ATTATAAAAA CAAAGTCAGA GCAGTCACTG GTGTCTGGGC ATGGAGGAGA 7260
AAGAAGAATT CTCTTCTCCC TTCACCCTCC ATGCCCTTTT TTGGCTCCAT GTGATTCAGA 7320
TTTCTGGACC CTGGAGCCCC ACCCCAAGCT AAAGACCAGG ATACAGGGAA GCCACAACCA 7380
CTGGCGGTTT TGAGAACTTA CTTTTCACCTT ATTCTGCATT TACTGTTTCC TTTTCTTATG 7440
CAGAAAAAGA AAAAAACCAA GGTAGGTGTG TGGGTAGAGA GCATGAAGTG TGTGTACTCA 7500
TGCATATGTA TGTGCATGCA TGTGAAGTGT GCATGTGTGA GCTCATATGC ATCCATGCAC 7560
CAGACTTGCC TCTTCCTCCC CCTCCTTCTT GAGCTTCTGC TGGGGCCGAG CGTGCAGTAA 7620
TGACAACTAC GATTTGCTGG GGGAAGGCTA CGTGCCAAGC ACTCTTTTAG GTGCTTTCCA 7680

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TGATTAATTC CTTCTCACA ACAGCCCTAT GAGATTAGTA CTATAACTAT CCCCATTTC 7740
AGAGGGAGAA AAGGTACAGA CTTGACTAAC TTGCCCAAGG CCACACAGCC AGAGAGGGGC 7800
AGAGCCAGTA CTTAGAGCCA GGCAGTCTGG GTCCAGAGTC CGTGTCTGA ACCACAAGAG 7860
GCCATCATAC GCCATCAGAT TTGGTGCTAG CATTCTGCTG GGTGCCTGGT GGTGATGGAT 7920
CCATCACAGG GGTCTCCAG GTACTGGTGC TGGCCAGAC CAGAGCTGAC ACTCCTCAGG 7980
CACTACCACA TTCCAGGCAC TGTGCTTGGG GTCAGTCCCT CTCTTTTTTT TCCCCCCAA 8040
TTATAACAGT ATCTACAAAG TAGGTGCTGT TATTTTCCC CTTTCACAGG TGAGATAGAC 8100
TCAAAGAAGT GAACTTGCCC AAGGAACAGA ACTAATGAGT GGGGAAAATG GAACTGGAAA 8160
CCATGTCTGT TTAATCCAAA ACCTGTGTTT CTTGCCCTCT TTCTCTGATG CCAGCCCCCT 8220
ACACTTCAAG GCCTGTGTTG TCCAGACCCA CACTCGGGCC TGCCAGTGTG TGCCTGGCAG 8280
GGATGCTCCA TGGCCACACC ATATCCATCC TACACATCCC CCCTCAGACT GTGACCTCCA 8340
TTTGCTCTGG GATCCCCACA AGCTTCAGCT GCTTGAGCAA GACACTGCTT AGAAGGCAGA 8400
GCAAGCCAAG GCCTCTGGGG CCTGCTGGGA GCCAAAGCTG GGGAGCCGT TCCACGGGTC 8460
TATCTGCTTG AGCTGTCTTA GATGAGCAGC ATGGAAGGGC AGTGGTGCAT GAGTCCAGGC 8520
GGGCTGCTTT TCTGCTCCGA GAGGCTCTGC CTGCCAGTT GTTCTCTGCA TTGCAGCCTC 8580
AATCCCCACA GCCTTGCTT CCCCCGGCTT TCCCTACAGG TGCACCGCAT CCACAGTGTT 8640
GGCACCATGC ACCAGCCGCT CTCCGTCTT TTCATATCCT TGTCACCTGC ACGAGCATGT 8700
CTTGAAAATA TCCCTTGTTT GTGTAGCATC TTAATGTTT TTGCAGTATG ATTTTGCATT 8760
CAGTATCTCA TTGATCCCC ACAAGAGCCC TATGAGGAGG GAAAGCAGAT TTAACATT 8820
AAGGATGAGT AACTGAGGC CAGAGAGGAT ATTTTGGTT TTTTGTAGA CAGTCTCACT 8880
CTGTCACCCA GCCTGGAGTG CAGTGGCTTG ATCTGGCTC ACTGCAAGCT CCACCTCCCA 8940
TGTTACACC ATTTTCCTGC CTCAGCCTCC CAAGTAGCTG GGAATACAGG CACCCACCAC 9000
CACACCCAGC TAATTTTTTT GTATCTTTAG TAGAGATGGG GTTTCACCCA GTTAGCCAGG 9060
ATGGTCTTGA TCTCTGACC TTGTGATCTG CCTGCTTCGG CCTCCTAAAG TGCTGGGATT 9120
ACAGGCGTGA ACCCCCCTGC CCGGCCAGAG AGGATATTTT TTAATGAGGG GCAGGGCTGG 9180
GATTCCAGCC CAGTGTCTG ATGGCTCACC CACTGACCAT TCCACTAATC CGTGTCTTT 9240
TTCAATCTAA ACTTTCAGGG TTGTAGAGGT TCCTTTGAGG TGCCTCAGTA CTTCCATGGT 9300

FIG. 8D/6

SUBSTITUTE SHEET (RULE 26)

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GATGTGGGGT CTGAGGGCCA AGAGCTCTGT TCTCATTAAT CAGAGAAGCT TGTGTTTTTA 9360
AAAACACCAT GTTACTGCA GGAAATTTAA TTGGACAGTG TTTCCATCTG GAAAAAAAAA 9420
AGTCTACAAA ATACTTGACA ATCACTGCAC TAGATCATGC TGCTTTTAGC ATTCTTAGCA 9480
TTTCACGTGC TGAGCTCTCA ATACTCTACC ATGAGGAGGG ATGGAGTGGG TATGAAAAGA 9540
TAAAGAACTG AAGTCACACG GCTTGTCAGT GGCAGAGATA GAGCTTGAAC CGAGGTTGAA 9600
GAGCTCCCGC CTATTCCTTT CCTCTTCTCA CTGGATAAAG CTGCTCCAAG AGAGGTGCTG 9660
CCTCAGTGTG CCTGTTTACA CTGTAATCCT CCCTTCCTTC CTGCCTCCTC CCTCCTCTCT 9720
CCAGCCCATC ATCTTCGTTT CGGACAGAGC AAACAGCAAC AAGGAGCTGG GTGTGGACCA 9780
GGAGTCAGAG GAGGGCAAAG GCAAAACAAG CCCTGATAAG CAAAAGCAGT CCCCACAGGT 9840
GTCTGGGCAT GTGGCATGGG TGGGGTGGCC AGCAGGCTAC AGGGGCTTCC TATGCGCTTG 9900
GGATACACAG GGGCTGGAGG CTTCCCAGGA GTTTGTCTTG AACATCTGGA GGTTTGAATT 9960
TGTCCCACTG ACCTTTTCTT TCAGCAAGTT CCCCTGAAAT TTGGGCTGCT GCTTGGGTGA 10020
ATATCCCAGG ATGGGGGTTT CATTCTAGGA GTGGACTGGC AGGCTGAGCC TCCCATGGAG 10080
CTGATCCAGC CAGGATACAG AGAAGGGGAG GCAAAGGCTG AGACAGAACC AGCTTGAGAG 10140
CGGAGGCGCA ACTCTTGTCT CCTGGTGGCC TTGAGCATTT CACAATAGGG GGATAAAGGA 10200
TAGGAGCAGA AAAGTGGGGC TGACTTCAGA AATGGGGTCC TCTAGAGCTC ACGGGAGGGT 10260
GTTAGATTGG AGTGGGAGCT TAGTGGAGGT GAGCCTTAGA GGCAAAAGTC TCCAGACCAA 10320
TCCAGGCCCC CTCTTCTATC CGGGGGCCCC TCTTCTATCC AGGGCCCCCTC TTCTGTCTGG 10380
GAGCCCCTCT TCTATCTGGG GCCTCATGCA GTGGGGCCTA GGGGAGGTTC TCTGAGGACT 10440
TGGCCTTGAT GACAGGGTGG CTGGAGGAAT CAGAACGGTC AGACCTTCTT TGACCTGCGG 10500
GCACCTTTAG TTGGAATGCT CAGGCCTGGG ATGGTGGAGG GGGCTCTTGC AGGTGGGGAC 10560
TGGGGTGGCG GGGAGGAGGC TGTATGGCCG CCATATCTCC TTTGGCTGGG GGCGTCAGGG 10620
CTGGAGAGGT GTGAAGAGTC CCTGAGGCCT CGATGCATCT CACTCCAGCT CACCAGGTCT 10680
GCATTTGCCC GTCCCCAGCT CCTGCTGCCA CCCCCGGCCG TTTTAGGCAC TTGGCTCCCT 10740
TGGCCCAGAG GAGCTTGCCCT CACAGGCCTG TGCACCTCTG ACCCCTGTGA ACCAGTTTTT 10800
CTTTGTGCCT CCACAGCCAC AGCCTGGCAA CTCTGATCAG GAAAGTGAGG AACAGCAACA 10860
ATTCCGGAAC ATTTTCAAGC AGATAGCAGG AGATGTGAGT ACCTCCAAGC CCAGGACGCC 10920

FIG. 8D/7

SUBSTITUTE SHEET (RULE 26)

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CACAGGTGCT TCCTTCTCTC CTGGATTAACT TGCTCAGATT ACCAATTATT TCATTATTGT	10980
TTGGTAGAGG TCACTTTTGA CTCGGTGGA GCCAGGGGAT GTGTGCGTAG CACACAAATC	11040
CACAAGCCCT TGAGTTTTGG ACTGCCACGT CTGCTGGGGG GCTCAGAGGC CTTTTTGCTC	11100
TGAGCTGCCC ACGGTGGTCC TGATAGCTGA GGTGCAGTAT CTGGCCCCCT GTCTTCCTCA	11160
GAAAAGCCCC AGCTTCCCAT GACATAATAG CACCGACAGG GATTTTACAA ACACAGCCAG	11220
GTGGAATTG TTTTGCAAAG TGTCCGCGCC AGGAGCTGCT GTACTCCTGA ACCATGACCC	11280
TCCTCTCCCT TCCTCCTCAG GACATGGAGA TCTGTGCAGA TGAGCTCAAG AAGGTCCTTA	11340
ACACAGTCGT GAACAAACGT GAGTTGCTCA AACCAAATGG GGGTGGGGTG GGTGGGGAGT	11400
CCCGTTGTCT CAAAGCAGCT CCTCACTCTT CTCCATCCCC CCAGACAAGG ACCTGAAGAC	11460
ACACGGGTTT CACTGGAGT CTGCGGTAG CATGATTGCG CTCATGGATG TATCCTTCCT	11520
GCCGCCCCCT CCGGACCCTC TGTCATCAGC CCACGGGGGC CAAGGCAACA TACAGGGTGC	11580
CCAGTCAGGC AAAGGGCCCT AATTGTGCTC CAGGGAACT TAAGGAGACC CTGATTCAGA	11640
ACATCTTGGA TACTCGTCTG AAAGGGGTTG TTAGAGGCGG AAGGGGAGGA TGTGGGTTG	11700
TAACTGCCCT AACCCCTGTG CTCTCTCAG GCCTGGGATC CTGCCCAAGC AAAAGTGGTC	11760
CTTAGGAGAG CGGCTCCTGG GTTACAGAGT AGGCGCAATC TCTGACTGGT GGTGGAGTGG	11820
AGGGGAGGGT TAAATAGTAC AACAGGGCAG TGGGTAGGAC AGCCCGGAGT CTCCTAGACC	11880
CTCCCTCCAA ATCCAGGGGG ATTTTGCTGT GTGCTGTGTA GCCCTGACCT CCCTCCTCCA	11940
GACAGATGGC TCTGGAAAGC TCAACCTGCA GGAGTTCCAC CACCTCTGGA ACAAGATTAA	12000
GGCCTGGCAG GTGGGAAGAG AAAATGAAGC GTGGGAGTCA AGAATGGGGT TGATTGAGAG	12060
ATTCAGTGTG TGACCTCCAT CCTCAAATTT TCTATTGCCA GAAAATTTTC AAACACTATG	12120
ACACAGACCA GTCCGGCACC ATCAACAGCT ACGAGATGCG AAATGCAGTC AACGACGCAG	12180
GTGCTGAGAA GGAAGGGGTG TCAGGGATGT GGACCCGAGA CGGTGGGAGC AGGAATGGGA	12240
GGGGACTAGC TACTAGGGCC CCACTAGAGA AGGAGAGGGA AAGGGCTTCT CACTTCCCT	12300
TCCCAGGTCA CAGAGTGTC GAGAGGCAGG GAAAATAGAA GACAGGCCCA AGGCCTCCAG	12360
CTCCACGTCC ACCTCTAACA TGGTCCCCTC CACAGGATTC CACCTCAACA ACCAGCTCTA	12420
TGACATCATT ACCATGCGGT ACGCAGACAA ACACATGAAC ATCGACTTTG ACAGTTTCAT	12480
CTGCTGCTTC GTTAGGCTGG AGGGCATGTT CAGTAAGTGG GAGAGGGGGG CTGCCCTCTG	12540

FIG. 8D/8

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CTCTCTTGCA GGGGCAGTTG TGGCAACAGG CATCTCACCT GATAATCTCC AGTCTGCTCC 12600
ATCCAGGCTG AACAAGGGCC AATGACCTCT TTAGGCCCAG AATGGGATGG CAAAGGGAGG 12660
GTTACTGGTG ATTCTCTGCC TGCACATCTT TGTGCTGATG AGGGACAGCA CTGGGCACAC 12720
GGTCCTCTGA GGGGAAGTTA CAGTAGTAGA GGCGGAGTGC GCCTGTAACT GGCCTCTGGC 12780
CTGTGCATTG TTTCACAGGA GCTTCTCATG CATTGACAA GGATGGAGAT GGTATCATCA 12840
AGCTCAACGT TCTGGAGGTA AAGCATAGGC ACAGCACATT CCCCTACAC ATTAAAACTC 12900
AAGGTGGAGG GGTCAACGGG GCGGACTGGA CCCAGGGTGT GCTCCTCATT TCCACACAGT 12960
GGTGGAGGGA AGGGATAGGA ACAGAACATG GAGGGAGGCT CAGCAGGCTC CCAGGACACA 13020
TGCACTTGAG GCCCAAAGG ACCTCTGCTC CCCAGTCAC TTGATGCGGG AAAACATGCA 13080
CCTTCTTAGG GAAGATCTAG GAGAAAGGAA ACAGTAAGCC ACTGCTTCTT GGAAAATCTT 13140
CTGGGGGTCT GACCTGCTGG GACTGTTCCC TTTCTCTTG CCCCGTAAGA TTCCTAGGGC 13200
GGGGGGGGG GGGGGTCACT CTTTCTGAT CTACATTCTG ATCTTGGGAC TTCTTTCAGT 13260
GGCTGCAGCT CACCATGTAT GCCTGAACCA GGCTGGCCTC ATCCAAAGCC ATGCAGGATC 13320
ACTCAGGATT TCAGTTTCAC CCTCTATTTT CAAAGCCATT TACCTCAAAG GACCCAGCAG 13380
CTACACCCCT ACAGGCTTCC AGGCACCTCA TCAGTCATGT TCCTCCTCCA TTTTACCCCC 13440
TACCCATCCT TGATCGGTCA TGCCTAGCCT GACCCTTTAG TAAAGCAATG AGGTAGGAAG 13500
AACAAACCCT TGTCCCTTTG CCATGTGGAG GAAAGTGCCT GCCTCTGGTC CGAGCCGCCT 13560
CGGTTCTGAA GCGAGTGCTC CTGCTTACCT TGCTCTAGGC TGTCTGCAGA AGCACCTGCC 13620
GGTGGCACTC AGCACCTCCT TGTGCTAGAG CCCTCCATCA CCTTCACGCT GTCCCACCAT 13680
GGGCCAGGAA CCAAACCAGC ACTGGGTTCT ACTGCTGTGG GTTAAACTAA CTCAGTGGA 13740
TAGGGCTGGT TACTTTGGGC TGTCCAATC ATAAGTTTGG CTGCATTTTG AAAAAAGCTG 13800
ATCTAAATAA AGGCATGTGT ATGGCTGGTC CCCTTGTGTT TTGTTGTCTC ACATTTAGAT 13860
ATCAGCCATG CATGACTGAA TGGCTTCCAA TCATATACTC ACCTATCACC TACAAGAGAA 13920
CAATGAAAAA CACACACAAA AACAAAATCT TGAATTTTGT AATCATGCCT ATTGCTATTT 13980
CTTGAGCATA AGAATGGCTC AGATACTTTC CAAGACATAA AAGGAAGGCA GAGGAATAGT 14040
TGTTGCTGTA AAAGACATCA AGAATAAATG GGGTCATGTA CAACGGGAGG GGCCGGTTAC 14100
CTGAATAATG GAGTGGAGAT TGAGCTATCC TAGCTCCTCT GCTCACTAAC TGACCTGTCC 14160

FIG. 8D/9

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CATGACCGTG GACAAAACCC TGAACGCAGC TGTITGTTTG CTAAACTTCT CTGGACCATG 14220
GCCTGCGGCA TATCTATAGG CATCCTGTGT TTTCCACCCA GTTTCCTTCT TCCTCGCTAA 14280
GCCAACGTGG AAAGGGCTGG CCGTGAATAT GCAGACAAGG TAACGAAAGT AAACCGTCAA 14340
TTAGTAAAAG TACTTCATTT TCCTCTTGTA TTTGCTTCAT TCTTGCTTCA CAAAGTTACG 14400
AAGTCCACAG CTTTATACCA AAATGTAAGA AGGCTATTTG CTTATAAACA TTTTGAGTCA 14460
GGTGTCACTT GATTTCAATC TTCTAATCCA TATTCAATAT TAAAAAATCA GAAACCAAGG 14520
GTGCTGGAGC AGCTCTAGGG CATATATTTT TCTTAAATAG GAGAAAGATT TTCAACAGCT 14580
TTTCCTCCTT GACCCCCTCC TTTCCCAATT TATTTGGGTC ACTACCTTGA ATTTAGAGTG 14640
AATCTGGGAA ATGTAGTCAC CAGG 14664

FIG. 8D/10

SUBSTITUTE SHEET (RULE 26)